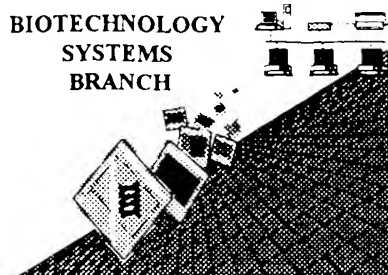


563)

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/018,311
Source: Pat/10
Date Processed by STIC: 1/9/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/018,311
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

PCT10

RAW SEQUENCE LISTING

DATE: 01/09/2002

PATENT APPLICATION: US/10/018,311

TIME: 13:53:13

Input Set : A:\ES.txt

Output Set: N:\CRF3\01082002\J018311.raw

5 <110> APPLICANT: MIYATA, Toshio
 7 KUROKAWA, Kiyoshi
 11 <120> TITLE OF INVENTION: Meg-3 protein
 15 <130> FILE REFERENCE: 2605/101
 19 <140> CURRENT APPLICATION NUMBER: US/10/018,311
 21 <141> CURRENT FILING DATE: 2001-10-30
 25 <160> NUMBER OF SEQ ID NOS: 8
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

953 <210> SEQ ID NO: 8
 955 <211> LENGTH: 29
 957 <212> TYPE: DNA
 959 <213> ORGANISM: Artificial Sequence
 963 <220> FEATURE:
 965 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
 967 Synthesized Primer Sequence
 971 <400> SEQUENCE: 8
 E--> 973 gcgaattcga actcagtcctg caccctctgc

29 ← insert cumulative base
 total at right margin
 of each line

see P. 3 for more error

10/018,311 2

<210> 1

<211> 3768

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(2251)

<400> 1

caggaactgg gccagctcgg gtcccttctt ttgggggtc tcactctgga gg atg ggg 58

Met Gly

1

tgg atg gga gaa aaa acc ggg aag atc ctg acg gag ttc ctc cag ttc 106

Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe

5

10

15

tat gaa gac cag tat ggc gtg gct ctc ttc aac agc atg cgc cat gag 154

Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg His Glu

20

25

30

att gag ggc acg ggg ctg ccg cag gcc cag ctg ctc tgg ccg aag gtg 202

Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg Lys Val

35

40

45

50

cca ctg gac gag cgc atc gtc ttc tcg ggg aac ctc ttc cag cac cag 250

Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln His Gln

55

60

65

(erroneous position of sequence 1)

10/018,311

3

ctggggagcc ggaagggggt cctgaggggt acaggttggg tgggcccctc ctgaggggtct 3231

ggggtcagga tttggcctct gctgcctctc agtcaccaag tcacctccct ctgaaaatcc 3291

agtcctttct ttggatgtcc ttgtgagtea ctctggggct ggetgtctgc cctctcagc 3351

ttcttgttcc tgggacaagg gtcaagccag gatggggcca ggctgggat cccccacccc 3411

aggacccccc agggcccctc cctgntgnt ttgogggggg cagggcagaa atggactcct 3471

tttgggtccc cgaggtgggg tcccctccca gccctgcac ctccgtgccc tagacctgct 3531

ccccagagga ggggccttga cccacaggaa gtgtgggtggc gccctggcaat cagggacccc 3591

cagctgcgcg agccctgggt tttggcgcat cttttccctc ttgtcccga gatttgcgcc 3651

tttagtgccct tttgaggggt tcccatcacc cctccctgat attgtattga aaatattatg 3711

cacactgttc atgcttttac taatcaataa acgctttatt taaaaaaaa aaaaaaa 3768

→ see
item 9
on
Error
Summary
Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/018,311

DATE: 01/09/2002

TIME: 13:53:14

Input Set : A:\ES.txt

Output Set: N:\CRF3\01082002\J018311.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
L:501 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:505 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:973 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:8